****
Reviewer Comments:
<210>   1
<211>   78
<212>   DNA
<213>   S. cerevisiae

<400>   1

GGAAT TCGGC ACCAT GTGCT TCTGT AAATA GTGTA TTGTG TTTTT AATGT   50
TGGAC TGGTT GGAAT AAAGC TCTAG AGC   78

For SEQ ID # 1 through 30 , "37 CFR 1.822 (c) Format representation of
nucleotides. (1) A nucleotide sequence shall be listed using the lower-
case letter for representing the one-letter code for the nucleotide
bases set forth in WIPO Standard ST.25 (1998) Appendix 2, Table 1."
Please make all necessary changes.

Nucleotide bases must be in groups of ten nucleotides, and maximum of 60
per line.

<210>   2
<211>   27
<212>   DNA
<213>   Artificial sequence
<223>   Primer directed to Aplysia cDNA

<400>   2

GCGGA ATTCG TNSAR GTNAT HCCNT GG

If the Numeric identifier <213> is "Artificial" there should be mandatory feature inserted which consists of numeric identifiers <220>, <221>, <222>, and <223>. Numeric identifier "<220> feature" should remain blank, numeric Identifier "<221> Name/Key" should be selected from "WIPO Standard ST.25 (1998), Appendix 2, Tables 5 and 6," numeric identifier "<222> Location" should "Specify location within sequence," and numeric identifier "<223> Other Information" should provide "Other relevant information, four lines maximum."

The sequence rules require that "the enumeration of nucleotide bases shall start at the first base of the sequence with 1. The enumeration shall be continuous through the whole sequence in the direction 5' to 3'. The enumeration shall be marked in the right margin, next to the line containing the one-letter codes for bases, and giving the number of the last base of that line." The enumeration is not marked in the right margin. Please check for the similar errors as sample shown above and make all necessary corrections.

* *

Application No: 10578203   Version No: 1.0

                Input Set:

                Output Set:

              Started: 2010-06-18 15:39:43.338
             Finished: 2010-06-18 15:40:05.747
              Elapsed: 0 hr(s) 0 min(s) 22 sec(s) 409 ms
      Total Warnings: 762
        Total Errors: 75
  No. of SeqIDs Defined: 30
   Actual SeqID Count: 30

Error code   Error Description

W   402   Undefined organism found in <213> in SEQ ID (1)

W   112   Upper case found in data; Found at position(0) SeqId(1)

W   112   Upper case found in data; Found at position(1) SeqId(1)

W   112   Upper case found in data; Found at position(2) SeqId(1)

W   112   Upper case found in data; Found at position(3) SeqId(1)

W   112   Upper case found in data; Found at position(4) SeqId(1)

W   112   Upper case found in data; Found at position(5) SeqId(1)

W   112   Upper case found in data; Found at position(6) SeqId(1)

W   112   Upper case found in data; Found at position(7) SeqId(1)

W   112   Upper case found in data; Found at position(8) SeqId(1)

W   112   Upper case found in data; Found at position(9) SeqId(1)

W   112   Upper case found in data; Found at position(10) SeqId(1)

W   112   Upper case found in data; Found at position(11) SeqId(1)

W   112   Upper case found in data; Found at position(12) SeqId(1)

W   112   Upper case found in data; Found at position(13) SeqId(1)

W   112   Upper case found in data; Found at position(14) SeqId(1)

W   112   Upper case found in data; Found at position(15) SeqId(1)

W   112   Upper case found in data; Found at position(16) SeqId(1)

W   112   Upper case found in data; Found at position(17) SeqId(1)

W   112   Upper case found in data; Found at position(18) SeqId(1)

```
                   Input Set:


                   Output Set:



              Started:   2010-06-18 15:39:43.338
             Finished:   2010-06-18 15:40:05.747
              Elapsed:   0 hr(s) 0 min(s) 22 sec(s) 409 ms
       Total Warnings:   762
         Total Errors:   75
  No. of SeqIDs Defined:   30
    Actual SeqID Count:    30
```

Error code	Error Description
W 112	Upper case found in data; Found at position(19) SeqId(1) This error has occured more than 20 times, will not be displayed
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (2)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 27 SEQID(2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (3)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 26 SEQID(3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (4)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 21 SEQID(4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (5)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 20 SEQID(5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (6)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 24 SEQID(6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)

```
                Input Set:


                Output Set:



            Started:    2010-06-18 15:39:43.338
           Finished:    2010-06-18 15:40:05.747
            Elapsed:    0 hr(s) 0 min(s) 22 sec(s) 409 ms
     Total Warnings:    762
       Total Errors:    75
No. of SeqIDs Defined:  30
  Actual SeqID Count:   30
```

Error code	Error Description
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (7)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 27 SEQID(7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (8)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 26 SEQID(8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (9)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 21 SEQID(9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (10)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 24 SEQID(10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (11)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 24 SEQID(11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (12)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 21 SEQID(12)

Input Set:

Output Set:

Started:	2010-06-18 15:39:43.338
Finished:	2010-06-18 15:40:05.747
Elapsed:	0 hr(s) 0 min(s) 22 sec(s) 409 ms
Total Warnings:	762
Total Errors:	75
No. of SeqIDs Defined:	30
Actual SeqID Count:	30

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (13)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 22 SEQID(13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (14)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 35 SEQID(14)
E 253	The number of bases differs from <211> Input: 37 Calculated:35
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (15)
E 330	Invalid protein , found in SEQID(15) POS (1)Invalid Protein:CGGGA
E 330	Invalid protein , found in SEQID(15) POS (2)Invalid Protein:TCCAT
E 330	Invalid protein , found in SEQID(15) POS (3)Invalid Protein:GCTGG
E 330	Invalid protein , found in SEQID(15) POS (4)Invalid Protein:ACAGC
E 330	Invalid protein , found in SEQID(15) POS (5)Invalid Protein:AACAA
E 330	Invalid protein , found in SEQID(15) POS (6)Invalid Protein:CAG
E 253	The number of bases differs from <211> Input: 28 Calculated:0
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (16)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 31 SEQID(16)

```
          Input Set:


          Output Set:



            Started:   2010-06-18 15:39:43.338
           Finished:   2010-06-18 15:40:05.747
            Elapsed:   0 hr(s) 0 min(s) 22 sec(s) 409 ms
     Total Warnings:   762
       Total Errors:   75
No. of SeqIDs Defined:   30
   Actual SeqID Count:   30
```

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (17)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 26 SEQID(17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (18)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 41 SEQID(18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (19)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 41 SEQID(19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (20)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 25 SEQID(20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21) This error has occured more than 20 times, will not be displayed
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (21) This error has occured more than 20 times, will not be displayed
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 24 SEQID(21)
E 331	Count of Protein differs from the <211> tag Input: 17
E 254	The total number of bases conflicts with running total Input: 0,

```
                  Input Set:


                  Output Set:



           Started:  2010-06-18 15:39:43.338
          Finished:  2010-06-18 15:40:05.747
           Elapsed:  0 hr(s) 0 min(s) 22 sec(s) 409 ms
    Total Warnings:  762
      Total Errors:  75
No. of SeqIDs Defined:  30
  Actual SeqID Count:  30
```

Error code	Error Description
	This error has occured more than 20 times, will not be displayed
E 330	Invalid protein , found in SEQID(29) POS (1)Invalid Protein:TTTGA
E 330	Invalid protein , found in SEQID(29) POS (2)Invalid Protein:GCATT
E 330	Invalid protein , found in SEQID(29) POS (3)Invalid Protein:CTGGC
E 330	Invalid protein , found in SEQID(29) POS (4)Invalid Protein:TTC
E 253	The number of bases differs from <211> Input: 18 Calculated:0
E 330	Invalid protein , found in SEQID(30) POS (1)Invalid Protein:AAACA
E 330	Invalid protein , found in SEQID(30) POS (2)Invalid Protein:GAGCA
E 330	Invalid protein , found in SEQID(30) POS (3)Invalid Protein:GGTCC
E 330	Invalid protein , found in SEQID(30) POS (4)Invalid Protein:CGGCA
E 330	Invalid protein , found in SEQID(30) POS (5)Invalid Protein:GAAAT
E 330	Invalid protein , found in SEQID(30) POS (6)Invalid Protein:AGT
E 253	The number of bases differs from <211> Input: 28 Calculated:0

<110> Kausik Si and Eric Kandel

<120> Prion-like form of CPEB and related compositions and methods

<130> 68103/JPW/BJA

<140> 10578203
<141> 2010-06-18

<150> PCT/US04/36781
<151> 2004-11-05

<150> 60/518,385
<151> 2003-11-07

<160> 30

<170> PatentIn version 3.3

<210> 1
<211> 78
<212> DNA
<213> S. cerevisiae

<400> 1

GGAAT TCGGC ACCAT GTGCT TCTGT AAATA GTGTA TTGTG TTTTT AATGT   50
TGGAC TGGTT GGAAT AAAGC TCTAG AGC   78

<210> 2
<211> 27
<212> DNA
<213> Artificial sequence
<223> Primer directed to Aplysia cDNA

<400> 2

GCGGA ATTCG TNSAR GTNAT HCCNT GG

<210> 3
<211> 26
<212> DNA
<213> Artificial sequence
<223> Primer directed to Aplysia cDNA

<400> 3

GCGGG ATCCT GNTGC CANTS CCARC A

<210> 4
<211> 21
<212> DNA
<213> Artificial sequence
<223> Primer directed to Aplysia mRNA

<400> 4

CACTG TCTTG TTCGA CTCCA G

<210> 5
<211> 20
<212> DNA
<213> Artificial sequence
<223> Primer directed to Aplysia mRNA
<400> 5

AACAC ATGGT TACTG TCCGC

<210> 6
<211> 24
<212> DNA
<213> Artificial sequence
<223> Primer directed to Aplysia mRNA

<400> 6

CATGA AAGCC GTGCA AGCTG CATT

<210> 7
<211> 27
<212> DNA
<213> Artificial sequence
<223> Primer directed to Drosophila melanogaster mRNA and cDNA

<400> 7

CGGGA TCCAT GTACA ACAAA TTTGT TA

<210> 8
<211> 26
<212> DNA
<213> Artificial sequence
<223> Primer directed to Drosophila melanogaster mRNA

<400> 8

TCCCC GCGGC GATCC TCCGC CTCCT C

<210> 9
<211> 21
<212> DNA
<213> Artificial sequence
<223> Primer directed to Drosophila melanogaster mRNA

<400> 9

ATGGA CTCGC TCAAG TTACC A

<210> 10
<211> 24
<212> DNA
<213> Artificial sequence
<223> Primer directed to Drosophila melanogaster mRNA

<400> 10

CGCGA TGCCT GATTG ATTGT TGAA

<210> 11
<211> 24
<212> DNA
<213> Artificial sequence
<223> Primer directed to Drosophila melanogaster mRNA

<400> 11

TGTGC GTTAT TTTAT CGTTT AGTG

<210> 12
<211> 21
<212> DNA
<213> Artificial sequence
<223> Primer directed to Drosophila melanogaster mRNA

<400> 12

GACTT CATCC GCCAC CAGTC G

<210> 13
<211> 22
<212> DNA
<213> Artificial sequence
<223> Primer directed to Drosophila melanogaster mRNA

<400> 13

CACCA GGAAC TTCTT GAATC CG

<210> 14
<211> 37
<212> DNA
<213> Artificial sequence
<223> Primer directed to Drosophila melanogaster cDNA

<400> 14

CCCTC GAGAA GCTTT TAACA CCAGC GAAAG GGGAC

<210> 15
<211> 28
<212> DNA
<213> Artificial sequence
<223> Primer directed to Drosophila melanogaster cDNA

<400> 15

CGGGA TCCAT GCTGG ACAGC AACAA CAG

<210> 16
<211> 31
<212> DNA
<213> Artificial sequence
<223> Primer directed to Drosophila melanogaster cDNA

<400> 16

GACTA GTCTA GAATA GATTA GCAAA GAAAT C

<210> 17
<211> 26
<212> DNA
<213> Artificial sequence
<223> Primer directed to Aplysia neuronal actin cDNA

<400> 17

GGGAA TTCGT CTGGA GCCAC CAACA C

<210> 18
<211> 41
<212> DNA
<213> Artificial sequence

<223>   Primer directed to Aplysia neuronal actin

<400>   18

CGGAT CCATT TATTA ACATT GTATA AAAAA TACAG TTGAA C

<210>   19
<211>   41
<212>   DNA
<213>   Artificial sequence
<223>   Primer directed to Aplysia neuronal actin

<400>   19

CGGAT CCATT TATTA ACATT GTATG GGAAA TACAG TTGAA C

<210>   20
<211>   25
<212>   DNA
<213>   Artificial sequence
<223>   Primer directed to Aplysia CPEB cDNA

<400>   20

CGGGA TCCAT GCAAG CCATG GCCGT

<210>   21
<211>   24
<212>   DNA
<213>   Artificial sequence
<223>   Primer directed to Aplysia CPEB cDNA

<400>   21

TCCCC GCGGT GGACC AGGCG TGTA

<210>   22
<211>   17
<212>   PRT
<213>   Artificial sequence
<223>   C-terminal peptide of CPEB (CPEB77)

<400>   22

LCNSH QGNYF CRDLL CF

<210>   23

<211> 30
<212> DNA
<213> Artificial sequence
<223> Primer directed to Aplysia RNA

<400> 23

GCGAG CTCCG CGGCC GCGTT TTTTT TTTTT

<210> 24
<211> 21
<212> DNA
<213> Artificial sequence
<223> Primer directed to Aplysia sensorin RNA

<400> 24

AACAG AAACA GTCTT TCCCC C

<210> 25
<211> 19
<212> DNA
<213> Artificial sequence
<223> Primer directed to Aplysia sensorin RNA

<400> 25

TCTTG ACTCA CCAAC TGCC

<210> 26
<211> 24
<212> DNA
<213> Artificial sequence
<223> Primer directed to Aplysia Bmp1 RNA

<400> 26

ATCTA TCGCC TATTA TTATC ACCA

<210> 27
<211> 20
<212> DNA
<213> Artificial sequence
<223> Primer directed to Aplysia Bmp1 RNA

<400> 27

ATCCC ATGCA TTTGT TTGTT

```
<210>  28
<211>  17
<212>  DNA
<213>  Artificial sequence
<223>  Primer directed to Aplysia N-actin RNA


<400>  28

CCCAT CCATT GTCCA CA



<210>  29
<211>  18
<212>  DNA
<213>  Artificial sequence
<223>  Primer directed to Aplysia N-actin RNA


<400>  29

TTTGA GCATT CTGGC TTC




<210>  30
<211>  28
<212>  DNA
<213>  Artificial sequence
<223>  Antisense oilgo directed to Aplysia CPEB mRNA


<400>  30

AAACA GAGCA GGTCC CGGCA GAAAT AGT
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